



Blast 2 Sequences results

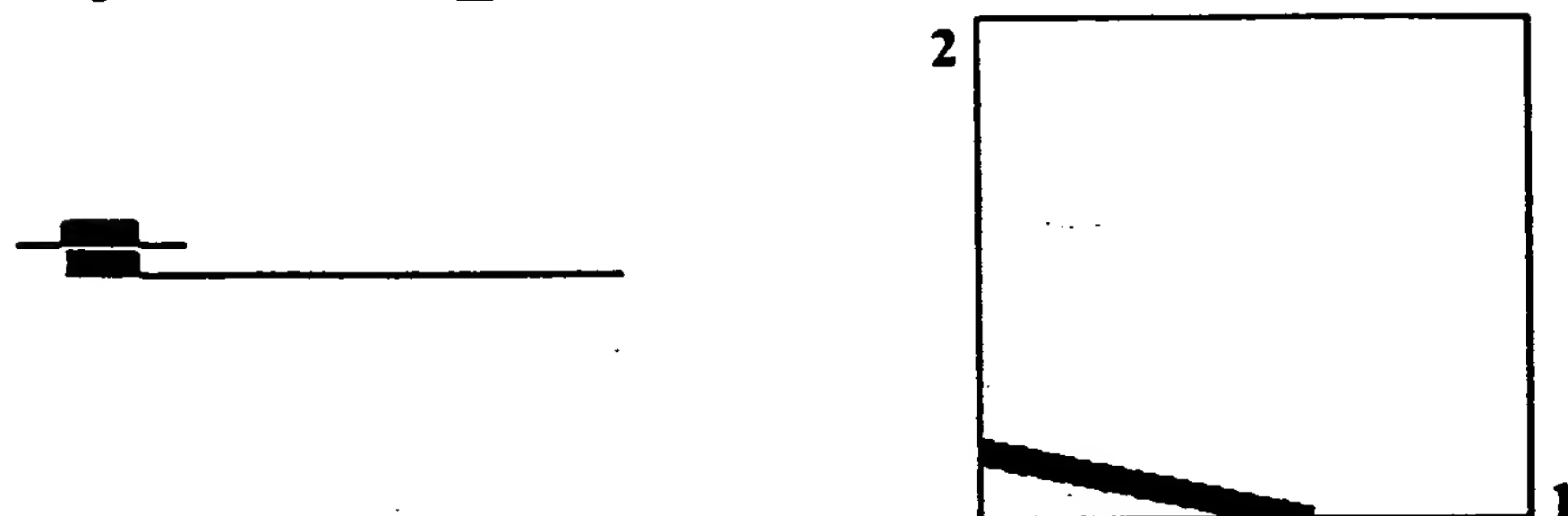
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BLAST 2 SEQUENCES RESULTS VERSION BLASTN 2.1.2 [Nov-13-2000]

Match: Mismatch: gap open: gap extension:
x_dropoff: expect: wordsize: ☐ Filter ☐ Align

Sequence 1 lcl|seq_1 Length 137 (1 .. 137)

Sequence 2 lcl|seq_2 Length 612 (1 .. 612)



NOTE: The statistics (bitscore and expect value) is calculated based on the size of nr database

Score = 148 bits (77), Expect = 5e-34

Identities = 81/83 (97%)

Strand = Plus / Minus

Query: 1 ccggttaagtaaacagtcagaaaattagcatgaaagcagtttagcattgggaggaagcaca 60
|||||
Sbjct: 85 ccggttaagtaaacagtcagaaaattagcatgaaagcagtttagcattgggaggaagctca 26

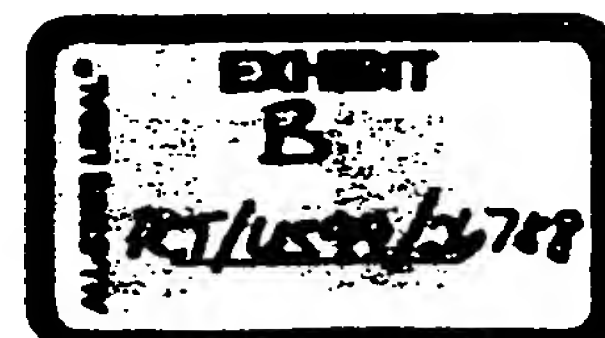
Query: 61 gatctctagagctgtcctgtcgc 83
|||||
Sbjct: 25 gatctctagagctgtcctgtcgc 3

CPU time: 0.02 user secs. 0.06 sys. secs 0.08 total secs.

Gapped
Lambda K H
1.33 0.621 1.12

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Matrix: blastn matrix:1 -2
Gap Penalties: Existence: 5, Extension: 2
Number of Hits to DB: 1
Number of Sequences: 0
Number of extensions: 1
Number of successful extensions: 1



Number of sequences better than 10.0: 1
length of query: 157
length of database: 2,635,864,967
effective HSP length: 22
effective length of query: 115
effective length of database: 2,635,864,945
effective search space: 303124468675
effective search space used: 303124468675
T: 0
A: 0
X1: 6 (11.5 bits)
X2: 26 (50.0 bits)
S1: 12 (23.8 bits)
S2: 18 (35.3 bits)